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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/930,906

TIME: 16:50:38

Input Set : A:\2363921.app

Output Set: N:\CRF3\08162001\I930906.raw

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3 <110> APPLICANT: Tarczynski, Mitchell C
4   Li, Changjiang
6 <120> TITLE OF INVENTION: Methods and Compositions for Modifying Oil and Protein
7   Content in Plants
9 <130> FILE REFERENCE: 5718-113 (35718/236392)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/930,906
C--> 12 <141> CURRENT FILING DATE: 2001-08-16
14 <150> PRIOR APPLICATION NUMBER: 60/226,142
15 <151> PRIOR FILING DATE: 2000-08-18
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2245
23 <212> TYPE: DNA
24 <213> ORGANISM: Zea mays
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35 gagcacgggg acatcaa atg gcg gca gcg gcg gag atc ggt ggt ttc gcg 170
36           Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala
37           1           5           10
39 gcg gcg aga gtg gcg gtg gca acg ctc agg ccg gct gcg cac cca gcc 218
40 Ala Ala Arg Val Ala Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala
41           15           20           25
43 ccg gcg gcg gcg gcg gca ccg cag cct agg agg gcg gtg gcg gcg cag 266
44 Pro Ala Ala Ala Ala Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln
45           30           35           40
47 tcg ctg cag acg acc gcc acc gag gcg ctg acg gcg gat ctc gcc ggc 314
48 Ser Leu Gln Thr Thr Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly
49           45           50           55
51 acg acc aac ggc gct gtg cat gct cgg atg aat agt aag gct aca agt 362
52 Thr Thr Asn Gly Ala Val His Ala Arg Met Asn Ser Lys Ala Thr Ser
53 60           65           70           75
55 gaa atc act tca cag gca gtt act gca aat tct agg aga aag aca aag 410
56 Glu Ile Thr Ser Gln Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys
57           80           85           90
59 ata gtc tgc acc ata ggt ccc tca acc aac act cgt gag atg att tgg 458
60 Ile Val Cys Thr Ile Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp
61           95           100          105
63 aag ctt gca gag act gga atg aat gta gcg cgc ctt aat atg tcc cat 506
64 Lys Leu Ala Glu Thr Gly Met Asn Val Ala Arg Leu Asn Met Ser His
65           110          115          120
67 ggt gac cac cag tcg cac cag aag gtt att gat ttg gtc aag gag tac 554
68 Gly Asp His Gln Ser His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr

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71	aat gca cag aac act gat ggc aat gtt att gcc att atg ctg gac aca	602		
72	Asn Ala Gln Asn Thr Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr			
73	140 145 150 155			
75	aag ggt cct gaa gtt aga agt ggg gat gtt cca gag cca atc atg ctc	650		
76	Lys Gly Pro Glu Val Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu			
77	160 165 170			
79	aag gaa ggt caa gag ttc aac ttc acg att aaa aga ggg gtg agc act	698		
80	Lys Glu Gly Gln Glu Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr			
81	175 180 185			
83	gaa gac act gtc agc gtg aac tat gat gac ttc ata aat gat gtt gaa	746		
84	Glu Asp Thr Val Ser Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu			
85	190 195 200			
87	gct ggc gac ata cta tta gtg gat gga gga atg atg tcg ctt gct gtg	794		
88	Ala Gly Asp Ile Leu Leu Val Asp Gly Gly Met Met Ser Leu Ala Val			
89	205 210 215			
91	aag tct aaa aca gcc gat aca gtc aag tgt aaa gta gtt gat ggt ggg	842		
92	Lys Ser Lys Thr Ala Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly			
93	220 225 230 235			
95	gaa ttg aaa tca cgg cgc cac cta aat gtc cgt gga aag agt gct act	890		
96	Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr			
97	240 245 250			
99	ttg cca tct atc act gag aag gat tgg gaa gac ata aaa ttt ggt gtc	938		
100	Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp Ile Lys Phe Gly Val			
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104	Glu Asn Gly Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys			
105	270 275 280			
107	gtt atc cat gaa tta aaa gac tac ctt aaa agt gct aat gcc gat ata	1034		
108	Val Ile His Glu Leu Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile			
109	285 290 295			
111	cat gtc att cca aaa att gaa agt gca gat tca ata cca aac ctg cag	1082		
112	His Val Ile Pro Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln			
113	300 305 310 315			
115	tcc att att gct gct tca gat ggg gca atg gtg gcg cgt gga gac ctt	1130		
116	Ser Ile Ile Ala Ala Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu			
117	320 325 330			
119	ggt gct gaa ctt ccg att gag gat gtt cct ttg cta cag gca gag att	1178		
120	Gly Ala Glu Leu Pro Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile			
121	335 340 345			
123	gtc caa aca tgt cga agc atg gag aaa cca gtc att gtc gct aca aat	1226		
124	Val Gln Thr Cys Arg Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn			
125	350 355 360			
127	atg ttg gaa agc atg att gac cat cct act ccc act agg gca gaa gtt	1274		
128	Met Leu Glu Ser Met Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val			
129	365 370 375			
131	tct gac ata gct att gca gtt cgg gaa ggt gct gat gcc atc atg tta	1322		
132	Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu			
133	380 385 390 395			

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136 Ser Gly Glu Thr Ala His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val
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139 atg cac act gtg gca ctc aga aca gaa tcc agc ctt tat aac cca act 1418
140 Met His Thr Val Ala Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr
141          415          420          425
143 act tct cct agt ctt gtt gca tct gca cag ggt cta cag aat gag gac 1466
144 Thr Ser Pro Ser Leu Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp
145          430          435          440
147 ttc tcc gca agc cag cta agt aaa atg ttc gga tct cat gca acg atg 1514
148 Phe Ser Ala Ser Gln Leu Ser Lys Met Phe Gly Ser His Ala Thr Met
149          445          450          455
151 atg gcc aac acc ctt cgc aca cca atc att gta ttt aca cag aca ggc 1562
152 Met Ala Asn Thr Leu Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly
153 460          465          470          475
155 tcc atg gct gtc ctc ctg agc cac tat cgt ccc tcg tct aca cta ttt 1610
156 Ser Met Ala Val Leu Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe
157          480          485          490
159 gca ttt aca aac gag gaa cga gtg aag caa cgg cta gca ctc tac cag 1658
160 Ala Phe Thr Asn Glu Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln
161          495          500          505
163 ggc gtc atc cct att cac atg cag ttc tct gac gac gca gaa gaa act 1706
164 Gly Val Ile Pro Ile His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr
165          510          515          520
167 ttc tcc aga gca att agc agc ttg ctg aaa gca caa tat gtg aag aag 1754
168 Phe Ser Arg Ala Ile Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys
169          525          530          535
171 gga gac tac gtc act ctt gtt cag agc gga gtg act tca atc tgg aga 1802
172 Gly Asp Tyr Val Thr Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg
173 540          545          550          555
175 gag gaa tcc act cac cac atc caa gtg agg aaa gtt cag gtc 1844
176 Glu Glu Ser Thr His His Ile Gln Val Arg Lys Val Gln Val
177          560          565
179 tgatgtgccg gtgggaattg gtcgtctgag aaattttgat agcgccgcct gatgtgttat 1904
181 catcattata tgtgtaattt tactgtttta ccaggagatt gctacgtcga gttatatgtt 1964
183 gtgtcgaatt cacgtgtagg ctctgaatct tgactgtgtt cgttcatttt cgcttgtttc 2024
185 acactgaagt gttataagct caactttact gcttttgttt tcttgtgaaa cttgagttta 2084
187 gtttcttggt acaaaaggag ctagcactaa cagggtggtg agttttgtaa acggggcgag 2144
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196 <212> TYPE: PRT
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199 <400> SEQUENCE: 2
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201 1 5 10 15
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204 20 25 30

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207          35          40          45
209 Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly Thr Thr Asn Gly Ala
210          50          55          60
212 Val His Ala Arg Met Asn Ser Lys Ala Thr Ser Glu Ile Thr Ser Gln
213 65          70          75          80
215 Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys Ile Val Cys Thr Ile
216          85          90          95
218 Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Thr
219          100          105          110
221 Gly Met Asn Val Ala Arg Leu Asn Met Ser His Gly Asp His Gln Ser
222          115          120          125
224 His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr Asn Ala Gln Asn Thr
225          130          135          140
227 Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr Lys Gly Pro Glu Val
228 145          150          155          160
230 Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu Lys Glu Gly Gln Glu
231          165          170          175
233 Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr Glu Asp Thr Val Ser
234          180          185          190
236 Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu Ala Gly Asp Ile Leu
237          195          200          205
239 Leu Val Asp Gly Gly Met Met Ser Leu Ala Val Lys Ser Lys Thr Ala
240          210          215          220
242 Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly Glu Leu Lys Ser Arg
243 225          230          235          240
245 Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr Leu Pro Ser Ile Thr
246          245          250          255
248 Glu Lys Asp Trp Glu Asp Ile Lys Phe Gly Val Glu Asn Gly Val Asp
249          260          265          270
251 Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys Val Ile His Glu Leu
252          275          280          285
254 Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile His Val Ile Pro Lys
255          290          295          300
257 Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln Ser Ile Ile Ala Ala
258 305          310          315          320
260 Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu Gly Ala Glu Leu Pro
261          325          330          335
263 Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile Val Gln Thr Cys Arg
264          340          345          350
266 Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn Met Leu Glu Ser Met
267          355          360          365
269 Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val Ser Asp Ile Ala Ile
270          370          375          380
272 Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu Ser Gly Glu Thr Ala
273 385          390          395          400
275 His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val Met His Thr Val Ala
276          405          410          415
278 Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr Thr Ser Pro Ser Leu

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279          420          425          430
281 Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp Phe Ser Ala Ser Gln
282          435          440          445
284 Leu Ser Lys Met Phe Gly Ser His Ala Thr Met Met Ala Asn Thr Leu
285          450          455          460
287 Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly Ser Met Ala Val Leu
288 465          470          475          480
290 Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe Ala Phe Thr Asn Glu
291          485          490          495
293 Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln Gly Val Ile Pro Ile
294          500          505          510
296 His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr Phe Ser Arg Ala Ile
297          515          520          525
299 Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys Gly Asp Tyr Val Thr
300          530          535          540
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324 ctctcctttg cttgcgcaga tctagcgc atg gcg gcg ggc ggt gag ttg gcg tgg 174
325          Met Ala Ala Gly Gly Glu Leu Ala Trp
326          1          5
328 ggg gag gag ccc gtg gcg cgg cgc cgg cct aag acc aag atc gtc tgc 222
329 Gly Glu Glu Pro Val Ala Arg Arg Arg Pro Lys Thr Lys Ile Val Cys
330 10          15          20          25
332 acg ctc ggc ccg gcg tcg cga tcc gtc gag atg atc tcg cgc ctg ctg 270
333 Thr Leu Gly Pro Ala Ser Arg Ser Val Glu Met Ile Ser Arg Leu Leu
334          30          35          40
336 cgc gcc ggg atg tgc gtc gcg cgc ttc aac ttc tcc cat ggc tcc cac 318
337 Arg Ala Gly Met Cys Val Ala Arg Phe Asn Phe Ser His Gly Ser His
338          45          50          55
340 gag tac cac cag gag acg ctc gac aac ctg cac gcc gcc atg gag ctc 366
341 Glu Tyr His Gln Glu Thr Leu Asp Asn Leu His Ala Ala Met Glu Leu
342          60          65          70
344 acc ggg atc ctc tgc gcc gtt atg ctc gac acc aag ggt cca gag att 414
345 Thr Gly Ile Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro Glu Ile
346          75          80          85
348 aga act gga ttt ttg aaa gat ggg aag cct att caa ttg ata aaa ggc 462
349 Arg Thr Gly Phe Leu Lys Asp Gly Lys Pro Ile Gln Leu Ile Lys Gly

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VERIFICATION SUMMARY

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Input Set : A:\2363921.app

Output Set: N:\CRF3\08162001\I930906.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date